

RESULT 1

Y938_MYCTU

ID Y938_MYCTU Reviewed; 759 AA.

AC P71571; O05865;

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 30-MAY-2000, sequence version 2.

DT 24-NOV-2009, entry version 67.

DE RecName: Full=Putative DNA ligase-like protein Rv0938/MT0965;

GN OrderedLocusNames=Rv0938, MT0965; ORFNames=MTCY08D9.01c, MTCY10D7.36c;

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium tuberculosis complex.

OX NCBI_TaxID=1773;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 25618 / H37Rv;

RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

RA Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,

RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RL Nature 393:537-544(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=CDC 1551 / Oshkosh;

RX MEDLINE=22206494; PubMed=12218036;

RX DOI=10.1128/JB.184.19.5479-5490.2002;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,

RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,

RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

RA Fraser C.M.;

RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";

RL J. Bacteriol. 184:5479-5490(2002).

CC -!- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.

CC -----

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CC -----

DR EMBL; BX842575; CAB08492.1; -; Genomic_DNA.

DR EMBL; AE000516; AAK45212.1; -; Genomic_DNA.

DR PIR; B70585; B70585.

DR RefSeq; NP_215453.1; -.

DR RefSeq; NP_335398.1; -.

DR PDB; 1VS0; X-ray; 2.40 Å; A/B=452-759.

DR PDB; 2IRU; X-ray; 1.65 Å; A/B=1-300.

DR PDB; 2IRX; X-ray; 1.80 Å; A=1-300.

DR PDB; 2IRY; X-ray; 1.78 Å; A/B=1-300.

DR PDB; 2R9L; X-ray; 2.40 Å; A/B=1-300.
 DR PDBsum; 1VS0; -.
 DR PDBsum; 2IRU; -.
 DR PDBsum; 2IRX; -.
 DR PDBsum; 2IRY; -.
 DR PDBsum; 2R9L; -.
 DR GeneID; 885561; -.
 DR GeneID; 926354; -.
 DR GenomeReviews; AE000516_GR; MT0965.
 DR GenomeReviews; AL123456_GR; Rv0938.
 DR KEGG; mtc:MT0965; -.
 DR KEGG; mtu:Rv0938; -.
 DR TIGR; MT0965; -.
 DR TubercuList; Rv0938; -.
 DR HOGENOM; P71571; --.
 DR OMA; VDWSQNN; -.
 DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-KW.
 DR GO; GO:0003910; F:DNA ligase (ATP) activity; IEA:InterPro.
 DR GO; GO:0003896; F:DNA primase activity; IEA:InterPro.
 DR GO; GO:0006310; P:DNA recombination; IEA:InterPro.
 DR GO; GO:0006281; P:DNA repair; IEA:InterPro.
 DR GO; GO:0006269; P:DNA replication, synthesis of RNA primer; IEA:InterPro.
 DR InterPro; IPR012309; DNA_ligase_A_C.
 DR InterPro; IPR012310; DNA_ligase_A_M.
 DR InterPro; IPR002755; DNA_primase_S.
 DR InterPro; IPR014144; LigD_PE_domain.
 DR InterPro; IPR014145; LigD_pol.
 DR InterPro; IPR012340; NA-bd_OB-fold.
 DR InterPro; IPR014146; NHEJ_ligase_lig.
 DR Gene3D; G3DSA:2.40.50.140; OB_NA_bd_sub; 1.
 DR Pfam; PF04679; DNA_ligase_A_C; 1.
 DR Pfam; PF01068; DNA_ligase_A_M; 1.
 DR Pfam; PF01896; DNA_primase_S; 1.
 DR TIGRFAMs; TIGR02777; LigD_PE_dom; 1.
 DR TIGRFAMs; TIGR02778; ligD_pol; 1.
 DR TIGRFAMs; TIGR02779; NHEJ_ligase_lig; 1.
 DR PROSITE; PS50160; DNA_LIGASE_A3; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; ATP-binding; Complete proteome; Ligase;
 KW Nucleotide-binding.
 FT CHAIN 1 759 Putative DNA ligase-like protein
 FT Rv0938/MT0965.
 FT /FTId=PRO_0000059627.
 FT ACT_SITE 481 481 N6-AMP-lysine intermediate (By
 FT similarity).
 FT CONFLICT 344 344 C -> R (in Ref. 2; AAK45212).
 FT TURN 20 22
 FT HELIX 26 44
 FT STRAND 50 53
 FT STRAND 63 65
 FT STRAND 76 83
 FT STRAND 86 92
 FT HELIX 96 104
 FT STRAND 109 112
 FT STRAND 114 119
 FT TURN 121 123
 FT STRAND 126 140

FT	HELIX	146	162
FT	STRAND	168	171
FT	STRAND	173	175
FT	STRAND	177	187
FT	HELIX	189	206
FT	TURN	208	210
FT	HELIX	217	219
FT	STRAND	221	227
FT	HELIX	229	231
FT	STRAND	246	248
FT	HELIX	257	260
FT	HELIX	270	280
FT	TURN	283	290
FT	HELIX	455	457
FT	STRAND	462	465
FT	TURN	473	475
FT	STRAND	476	479
FT	STRAND	484	492
FT	STRAND	495	500
FT	HELIX	507	509
FT	HELIX	511	513
FT	HELIX	514	519
FT	TURN	520	522
FT	STRAND	524	532
FT	HELIX	542	546
FT	STRAND	555	564
FT	HELIX	574	587
FT	HELIX	600	609
FT	STRAND	614	619
FT	STRAND	629	650
FT	STRAND	662	669
FT	STRAND	672	679
FT	HELIX	685	695
FT	HELIX	696	698
FT	STRAND	704	707
FT	HELIX	711	714
FT	STRAND	717	720
FT	STRAND	725	731
FT	STRAND	743	747
FT	HELIX	753	755
SQ	SEQUENCE	759 AA;	83572 MW; 81BD49222EE09E36 CRC64;
Query Match 100.0%; Score 3993; DB 1; Length 759;			
Best Local Similarity 100.0%;			
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MGSASEQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVMLGHIAGRPATRKWPNGVDQ	60
Db	1	MGSASEQRVTLTNADKVLYPATGTTKSDIFDYYAGVAEVMLGHIAGRPATRKWPNGVDQ	60
Qy	61	PAFFEKQLALSAPPWLSRATVAHRSGTTTYPIDIIDSATGLAWIAQQAALEVHVPQWRFVAE	120
Db	61	PAFFEKQLALSAPPWLSRATVAHRSGTTTYPIDIIDSATGLAWIAQQAALEVHVPQWRFVAE	120
Qy	121	PGSGELNPGPATRLVFDDPGEGVMMAQLAEVARAVRDLLADIGLVTFPVTSGSKGLHLY	180
Db	121	PGSGELNPGPATRLVFDDPGEGVMMAQLAEVARAVRDLLADIGLVTFPVTSGSKGLHLY	180

Qy	181	TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMKSRLAGKVFVDWSQNSGSKTTIAP	240
Db	181	TPLDEPVSSRGATVLAKRVAQRLEQAMPALVTSTMKSRLAGKVFVDWSQNSGSKTTIAP	240
Qy	241	YSLRGRTHPTVAAPRTWAELDDPALRQLSYDEVLTRIARDGDLLERLDADAPVADRLTRY	300
Db	241	YSLRGRTHPTVAAPRTWAELDDPALRQLSYDEVLTRIARDGDLLERLDADAPVADRLTRY	300
Qy	301	RRMRDASKTPEPIPTAKPVTGDGNTFVIQEHHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Db	301	RRMRDASKTPEPIPTAKPVTGDGNTFVIQEHHARRPHYDFRLECDGVLVSWAVPKNLPDN	360
Qy	361	TSVNHLLAIHTEDHPLEYATFEGAIPSGEYGAGKVIIWDSGYDTEKFHDDPHTGEVIVNL	420
Db	361	TSVNHLLAIHTEDHPLEYATFEGAIPSGEYGAGKVIIWDSGYDTEKFHDDPHTGEVIVNL	420
Qy	421	HGGRISGRYALIRTNGDRWLAHRLKNQKDQKVFEFDNLAPMLATHGTVAGLKASQWAFEG	480
Db	421	HGGRISGRYALIRTNGDRWLAHRLKNQKDQKVFEFDNLAPMLATHGTVAGLKASQWAFEG	480
Qy	481	KWDGYRLLVEADHGAVRLRSRSGRDVTAEYPQLRALAEDLADHHVLDGEAVVLDSSGVP	540
Db	481	KWDGYRLLVEADHGAVRLRSRSGRDVTAEYPQLRALAEDLADHHVLDGEAVVLDSSGVP	540
Qy	541	SFSQMQRGRDTRVEFWAFDLYLDGRALLGTRYQDRRKLLLETLANATSLTVPELLPGDG	600
Db	541	SFSQMQRGRDTRVEFWAFDLYLDGRALLGTRYQDRRKLLLETLANATSLTVPELLPGDG	600
Qy	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV	660
Db	601	AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV	660
Qy	661	GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAGITYV	720
Db	661	GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAGITYV	720
Qy	721	KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE	759
Db	721	KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE	759

RESULT 1

B70585

hypothetical protein Rv0938 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: B70585

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537–544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.

A; Reference number: A70500; MUID: 98295987; PMID: 9634230

A;Accession: B70585

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A; Residues: 1-759

A;Cross-references: UNIPROT:P71571; UNIPARC:UPI0000139E3C; GB:Z95209; GB:AL123456;
NID:g3261750; PIDN:CAB08492.1; PID:e1299776; PID:g3261755

A:Experimental source: strain H37By

H, Experimental source: Serial numbers C:Genetics:

Gene: Env

A; Gene: Rv0950

Query Match 100.0%; Score 3993; DB 2; Length 759;
Best Local Similarity 100.0%;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSASEQRVTLTNADKVLYPATGTTSDIFDYYAGVAEVMLGHIAGRPATRKRWPNGVDQ 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 PAFFEKOLALSAPPWLSRATVAHRSGTTTYPIDIIDSATGLAWIAOOAALEVHVPOWRFVAE 120

Pb 61 PAFFEKOLALSAPPWL SRATVAHRSGTTTYPIDSATGLAWIAOOAALEVHVPOWRVAE 120

Qy 121 PGSGELNP GPATRLVFDLDPGEGVMMAQLAEVARV DLLADIGLVT FPVT SGSK GLHLY 180

Db 121 PGSGELNP GPATRLVFDLDPGEGVMMAQLAEVARAVR DLLADIGLVTFPVTSGSKGLHLY 180

QY 181 IPILEPVSSRGATIVLAKRVAQRLEQAMPALVISIMIKSLRAGKVFVDSQNSGSKIIAP 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Pf 181 TRI DEPVSSRGATIVLAKRVAQRLEQAMPALVISIMIKSLRAGKVFVDSQNSGSKIIAP 240

181 TPLDEPVSSRGATVLAKKVVAQRLEQAMPALVISIMIKSLRAGKVFVDWSQNNSGSKITIAP 240

QY 241 YSLGRHTHP1VAAPR1WAELDDPALRQLSYDEV1R1ARDGDLLE1R1DADAPVADR1RY 300
P1 241 YSLGRHTHP1VAAPR1WAELDDPALRQLSYDEV1R1ARDGDLLE1R1DADAPVADR1RY 300

Db 241 YSLRGRTPTVAAPRITWAELDDPALRQLSYDEVLRTRIARDGDLLELDADAPVADRLTRY 300

Db 301 RRRMRDASKTPEPIPTAKPVTGDGNTFVIOEEHHARRPHYDFRLECDGVLVSWAVPKNLPDN 360

Pb 361 TSVNH LAIHTEDH PLEYAT FEEGA IPSGEY GAGKVI IWDSGTYDTEKEH DDDPHTGEVIVNL 420

421. UCCBISCBVALIPTNGDPWLNURJKNOKDQKVEERDNLADMILATTCVUGLKAQOMAEEG. 400

Db 421 HGGRISGRRALIRTNQDRWLARLKNQKDQKVFEFDNLAPMLATHGTVAGLKASQWAFEG 480

Db 481 KWDGYRLLVEADHGAVRLRSRSGRDVTAEYPQLRALAEDLADHHVVLGEAVVLDDSGVP 540

|||||

Db 541 SFSQMQRGRDTRVEFWAFDLYLDGRALLGTRYQDRRLLETLANATSLTVPELLPGDG 600
Qy 601 AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV 660
|||
Db 601 AQAFACSRKHGWEGVIAKRRDSRYQPGRRCASWVKDKHWNTQEVVIGGWRAGEGGRSSGV 660
Qy 661 GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV 720
|||
Db 661 GSLLMGIPGPGLQFAGRVTGLSERELANLKEMLAPLHTDESPFDVPLPARDAKGITYV 720
Qy 721 KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE 759
|||
Db 721 KPALVAEVRYSEWTPEGRLRQSSWRGLRPDKKPSEVVRE 759